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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                      Post-processing:
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                                                                                                                                                                                        SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria
   10:
11:
12:
13:
14:
                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                 425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-483-543A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         September 27, 2001, 16:40:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRGCAGNEDSEERSSWYWGR.....QQNPDEDFSGCGXGLEVLFQ 318
                                                                               sp_phage: *
                                                                                                                                                                                                       sp_archea:*
                                                                                            sp_organelle:*
                                                                                                                                                                                           sp_bacteria:*
                                                                                                                                                                           sp_fungi:*
                                                                                                              sp_mhc:*
                                                                                                                         sp_mammal:*
                                                                                                                                             sp_invertebrate:*
                                                                                                                                                            sp_human:*
sp_virus:*
                sp_unclassified:*
sp_vertebrate:*
                                               sp_rodent:*
                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Search time 38.23 Seconds (without alignments) 1100.523 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                   425026
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	ъ	4	ω	2	1	NO.	Result	
161	161	162	162	163	163.5	164	165	170	173	173	182	184.5	193	200	213	343	834.5	1078	Score	١	
9.5	9.5	9.6	9.6	9.6	9.7	9.7	9.7	10.0	10.2	10.2	10.8	10.9	11.4	11.8	12.6	20.3	49.3	63.7	Match I	Query	d
1097	1094	1217	815	684	857	1196	1270	816	666	640	1097	1010	1067	600	217	279	255	239	ength		
5	Ģ	11	4	4	ω		13	4	4	4		13	13	G	13	ഗ	14	11	DB	l	
Q9VIF7	061618	Q9WVE9	Q9P2Q0	Q9Y338	Q9P7E8	035413	042287	Q9UFT2	060592	060593	Q9U2T9	Q9YHU7	д9тни6	Q9VE96	Q9PU11	Q9NHC3	Q99059	Q9QW60	ID		
Q9vif7 drosophila	061618 drosophila	Q9wve9 rattus norv	Q9p2q0 homo sapien	Q9y338 homo sapien	Q9p7e8 schizosacch	035413 rattus norv	042287 xenopus lae	Q9uft2 homo sapien	060592 homo sapien	O60593 homo sapien		Q9yhu7 xenopus lae	Q9yhu6 xenopus lae	Q9ve96 drosophila	Q9pu11 xenopus lae	Q9nhc3 caenorhabdi	Q99059 avian sarco	Q9qw60 mus sp. grb	Description		

Qy Qy

33

5

65 INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS 124

AGNEDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
150.5	151	151	151.5	152	152.5	153	154	154.5	154.5	154.5	155	156	156.5	156.5	157	157	157	157	157.5	158	158	159	159	160	161
8.9	8.9	8.9	8.9	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.2	9.2	9.2	9.2	9.3	9.3	9.3	9.3	9.3	9.3	9.3	9.4	9.4	9.5	9.5
687	1186	1146	334	954	1011	1714	825	724	714	684	505	939	500	330	1696	1681	1676	1248	820	1220	1004	1721	1220	1721	1100
11	G	1	σ	σ		11			11		σı	σ	σı	4	4	4	4	4	11	4	4	4	4	4	4
Q9QY53	061080	Q9WVE1	Q9TYT3	097180	061639	Q9Z0R4	075815	Q9Z0Z9	Q9Z0Z8	Q62417	097337	Q24145	Q9 V 5J3	Q9NRB7	Q9NZM3	Q9NYG0	Q9ULG4	Q9NZM2	Q9QZK2	Q9UNK1	Q9UHN7	Q9UNK2	Q9UET5	095216	094875
Q9qy53 mus musculu	O61080 acanthamoeb	Q9wvel rattus norv	Q9tyt3 caenorhabdi	097180 drosophila	061639 drosophila	Q9z0r4 mus musculu	075815 homo sapien		Q9z0z8 mus musculu	Q62417 mus musculu	097337 paracentrot	Q24145 drosophila	Q9v5j3 drosophila		homo	Q9nyg0 homo sapien	Q9ulg4 homo sapien	Q9nzm2 homo sapien	Q9qzk2 mus musculu	Q9unk1 homo sapien	Q9uhn7 homo sapien	Q9unk2 homo sapien	Q9uet5 homo sapien	095216 homo sapien	094875 homo sapien

ALIGNMENTS

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Query Match
Best Local S
Matches 206
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Q9QW60;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                         MEDLINE-93028373; PubMed-1409582;
MEDLINE-93028373; PubMed-1409582;
MEDLINE-93028373; PubMed-1409582;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GRB-3-EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.
                                                                                                                                                                  Proc. Natl. Acad. Sci. U
HSSP; Q64010; 1CKA.
InterPro; IPR000980; -.
InterPro; IPR001452; -.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                    "High-efficiency expression/cloning of epidermal growth factor-receptor-binding proteins with Src homology 2 domains."; proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).
                                                              SEQUENCE
                                                                         PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                               Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                   Mus sp.
Local Similarity
nes 206; Conserv
                                                              239 AA; 26013 MW;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
          63.7%;
0;
Score 1078; DB 11;
Pred. No. 8.6e-82;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                              48326D680C9F09B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               239
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  Indels
                        Length 239;
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 Gaps
  0;
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Best Local
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HSSP; Q64010; ICKA.
InterPro: IPR000980; --
InterPro: IPR001452; --
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Q99059;
Q99059;
Q1-NOV-1996 (TIEMBLrel. 01, 01-NOV-1996 (TIEMBLrel. 16, 01-MAR-2001 (TIEMBLrel. 16, 01-MAR-2001 (TIEMBLREL)).
                                                                                                                                                                        DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                          Oncogene;
                                                                                                                                                                                                                                          SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                  Oncogene 4:1281-1284(1989).
                                                                                                                                                                                                                                                                                                                                                  oncogene.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=90045469; Tsuchie H., Chang
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11957;
                                                                                                                                                                                                                                                                                                                                                                                                           Avian sarcoma virus 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299059
                                                                                                                                                                                                                                                                                                                                                             "A newly
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232
               184
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       MIPVPYVEKYRPASASVSALIGG
                                                                                               | IPVPYVEKYRPASASVSALIGGNQEGS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIPVPYVEKCRPSSASVSTLTGG
                               SRQNSGVILRQEEVEYVRALFDFNGNDDEDLPFKKGDILKIRDKPEEQWWNAEDMDGKRG
                                        SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG
                                                                VNSLGPAGGRRAGGEGPGAPGLNPTRFRIGDQEFDSLPSLLEFYKIHYLDTTTL1EPVSR
                                                                        INSSGPRPPVPPSPAQP-PPGVSPSRLRIGDQEEDSLPALLEFYKIHYLDTTTLIEPVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPVPYVEKYRPASASVSALIGGNQEGS
                                                                                                                                  159;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                      90045469; PubMed=2554234;
H., Chang C.H.W., Yoshida M.,
isolated avian sarcoma virus,
                                                                                                                                                                                                                                  Polyprotein;
                                                                                                                                                                         1
<1
24
63
188
254
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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253
112
239
255
27985
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78
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                                                                                                                                        MW.
                                                                                                                                b; Score 834.5;b; Pred. No. 1.5e17; Mismatches
                                                                                                                                                                                                                                  domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                       GAG (BY SIMILARITY).
CRK (BY SIMILARITY).
SH2 (OR B+C BOX) (BY SIMILARITY).
SH3 (OR A BOX) (BY SIMILARITY).
GAG (BY SIMILARITY).
; 0C562D0B23Z7A579 CRC64;
254
               206
                                                                                                                                                                                                                                                                                                                                    EACH
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                                                                                                                                                                                                                                  SH2 domain.
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, ASV-1, ca
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                                                                                                                                                                                                                                                                                                                                                                                                           Avian type C
                                                                                                                                1.5e-61;
hes 26;
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on update)
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                                                                                                                                                                                                                                                                                                                                    SH2
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                                                                                                                                 Indels
                                                                                                                                                 Length
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                                                                                                                                 Gaps
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                                233
                                                183
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RESOLT

Q9NHC3

ID MC3

AC Q9

DT DT Q0

OC GN C C Q9

RT RN

RT RN

RT RN

DDR

DDR

DDR

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RESULT ID PU11 OF PU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 93
                                      Eukaryota; Metazoa; Ch
Amphibia; Batrachia; A
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NHC3;
01-OCT-2000
01-OCT-2000
                                                                                                                                Q9PU11;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                         GRB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SEQUENCE 279 AA; 30878 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NHC3
    Goisset C.,
                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                       11na60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000980; InterPro; IPR001452; Pfam; PF00017; SH2; 1. Pfam; PF00018; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Cell Biol. 0:0-0(2000)
EMBL; AF226866; AAF33845.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reddien P.W., Horvitz H.R.;
"CED-2/CrkII and CED-10/Rac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CED-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001
  SEQUENCE FROM N. Goisset C., Shi
                                                                                                                                                                                                                                                          214
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                                                                                                                        PROTEIN.
                                                                                                                                                                                                                                                          QPRLPAKAKVTFDRVPNAYDPTQLRVKKGQTVLVTQKMSNGMYKAELDGQIGSVPHTYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                    HYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDSEERSSWYWGRLSRQEAVALLQGQRH----GVFLVRDSSTSPGDYVLSV----SENSRVS
                                                                                                                                                                                                                                                                                                                                                                                                                     HYLIERGEPK-----EDGTAAAGVKIANQSFPDIPALLNHFKMRVLTEASLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDPFEWRSFYFPGMSREEAHKLL-GEPQVSIGTFLMRDSS-RPGEYSLTVREADEGNAVC
                                                                                                                                                                                                                                                                                  -- NGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVR
                                                                                                                                                                                                                                                                                                              TGLVPANYVQIQMEFHNDRTS---
                                                                                                                                                                                                                                                                                                                                      RGMIPVPYVE----KYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQ-
                                                                                                                                                                                                                                                                                                                                                                                           ARSRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                 ----AAYKKPIIEVVVGTFKFTGERETDLPFEQGERLEILSKTNQDWWEARNALGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TYEMBLrel. 15, Created)
(TYEMBLrel. 15, Last sequence u)
(TYEMBLrel. 16, Last annotation
ENGULFMENT PROTEIN CED-2.
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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    D A
    .L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.3%;
  Boucaut
                                                                                                                                   13,
13,
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                                                                                                                                   Created)
Last sequence update)
Last annotation updat
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.9e-21;
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on update)
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barlie C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayatktaroglu L., Beasley E.M.,
Bellew R.M., Basu A., Baxendale J., Bayatktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenort L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenort L.B., Davies P.,
A Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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Best Local
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Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SMART; SM00326; SH3; 1.
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01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by interfering mutants of Sem-5/Grb2.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ
EMBL; AJ223061; CAB59279.1;
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG7129 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VE96;
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                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                MEDIINE=20196006; PubMed=10731132;
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K., Doup L.E., Downes M.,
K.J., Evangelista C.C., F.
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1 (TrEMBLrel.
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Last sequence up
Last annotation
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Pred. No. 4
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A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Shue B.C., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Lang Y., Zhong W., Zhou S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
The genome sequence of Drosophila melanogaster.";
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Best Local Similarity
                                                                                             09YHU6;
01-MAY-1999
01-MAY-1999
01-MAR-2001
               01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHOLIPASE C-GAMMA-1B (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000).
EMBL; AE003721; AAF55531.1; -.
HSSP; P29354; 1GFC.
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                                                                                                                                                                        90HH06
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                                                                                                                                                                                                                                                                                                          THVRLLDQ 299
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                                                                                                                                                                                                                                                                     592
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Pred.
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H.O.,
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Matches 95
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PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0421; SH3DOMAIN.
PROMESTE; PRO0422; SH3DOMAIN_2; 1.
PROSITE; PS50004; C2_DOMAIN_1: 1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50007; PIFLC_X_DOMAIN; 1.
PROSITE; PS50008; PIFLC_X_DOMAIN; 1.
PROSITE; PS50001; SH2; 2.
PROSITE; PS50001; SH3; 1.
SMART; SM00239; C2; 1.
SMART; SM00239; C2; 1.
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Interpro; IPR000909; ...
Interpro; IPR000980; ...
Interpro; IPR001980; ...
Interpro; IPR00142; ...
Interpro; IPR00142; ...
Interpro; IPR00171; ...
Interpro; IPR002048; ...
Pfam; PF00018; SH3; 1.
Pfam; PF00018; SH3; 1.
Pfam; PF00168; C2; 1.
Pfam; PF00169; PH-PLC-Y; 1.
Pfam; PF00387; PI-PLC-Y; 1.
Pfam; PF00388; PI-PLC-Y; 1.
PRNNTS; PR00390; PHPHLIPASEC.
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---YDKTALALEVGELV
                                                  APRODVHNGRPFVFTITGPQLNRYPLDVAADTLEDMQD---WIRKIREAAQTADARLTEG
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                                                                                                  --NQEGSHPQP----LGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNA-----
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                                                                                                                                                                                                  EEQWWNAEDSEGKRGM-IPVPYVEK-YRPA-----
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                                                                                                                                                     EGGWWRG-DCGGKKQMWFPANYVEEIFSPAEPEPERQNLDENSPLGDLLGGVLDVPSCHI
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95; Conservative
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21.78;
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Pred. No. 1.6e-07;
3; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533F6876ECDFE5DB CRC64;
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InterPro; IPRO01452; ...
InterPro; IPRO01112; ...
InterPro; IPRO01711; ...
InterPro; IPRO01712; ...
InterPro; IPRO01720; ...
InterPro; IPRO01720; ...
InterPro; IPRO01849; ...
Pfam; PF00016; SH3; 1.
Pfam; PF00016; CC; 1.
Pfam; PF00168; CC; 1.
Pfam; PF00189; PH; 2.
Pfam; PF00387; PI-PLC-Y; 1.
Pfam; PF00388; PI-PLC-Y; 1.
Pfam; PF00388; PI-PLC-Y; 1.
Pfam; PF00389; PHPHLIPASEC.
PRINTS; PR00401; SH3DOMAIN.
PRINTS; PR00401; SH3DOMAIN.
PRINTS; PR00401; SH3DOMAIN.
PROSITE; PS50004; CC_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1
PROSITE; PS50001; SH3; 1.
SMART; SM00252; SH3; 1.
SMART; SM00252; SH3; 1.
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SEQUENCE
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Kung H.-F., Kim J., Huang Y.K., Lin
Molecular cloning of two different
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01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-MAR-2001 (TIEMBLIEL 116, Last annotation update)
PHOSPHOLIPASE C-GAMMA-1A (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YHU7;
01-MAY-1999
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NCBI_TaxID=8355;
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498 SFRAEGKIKHCRVIQEGQSVVLGSSEFDSLVDLISYYEKHPLYRKMKLRYPINEETLEKI
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                                                                                                                                                                                                        VRESETFYGDYTLSFWRNGKVQHCRIHSRQEAGSPKFFLTDNLVFESLYALITHYQQMPL 437
                                                                                                                                                                                                                                                                                                        GNQANDDEEEQKEASNSSELHSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGAPDGSFL
                                                                                                  RCNEFEMRLTEPYPQTNAHESKEWYHASLTRGQAEHMLMRVPRDGAFLVRKRSEQNSYAI
                                                                                                                                                     -----PPVPPSPAQ-----
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84; Conservative
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1010 AA;
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                                                  · IGDQEFDSLPALLEFY - ·
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Pred. No. 7.6e-07
28; Mismatches 10
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InterPro; IPRO00108; -.
InterPro; IPR000261; -.
InterPro; IPR000261; -.
InterPro; IPR001452; -.
InterPro; IPR002048; -.
InterPro; IPR002048; -.
Pfam; PF00018; SH3; 5.
Pfam; PF00018; Gefhand; 2.
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O9U2T9;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, L
O1-MAR-2001 (TrEMBLrel. 16, L
Y116A8C.36 PROTEIN.
Y116A8C.36.
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PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS00152; ATPASE_ALPHA_BETA;
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS50002; SH3; 5.
SMART; SM00054; EFh; 1.
                                                                                                                                                                                                                                                                                                                                                                investigating biology,";
Science 282:2012-2018(1998).
-; SIMILARITY: TO EF-HAND FAMILY.
EMBL, AL117204; CAB55138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditidae; Peloderinae; NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                       Calcium-binding.
SEQUENCE 1097 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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  747
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MPPNMTPSSSVDQIGVKAARKAEIAAA---
                    SPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEE
                                         RSEDELSFEPGDVIIVFQSHAAEPGWRAGQLREKVGWFPEAFVEAIAAVPTPGGDPPIQN
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                                                                                                                                 Similarity 21.: 75; Conservative
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                                                               STSPGDYVLSVSENS-----
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Last sequence update)
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5; Mismatches
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MGLTEGGAPPASSAPAAAAVISQCI
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InterPro; IPR001452; ...
InterPro; IPR003127; ...
InterPro; IPR003127; ...
Pfam; PF00208; Su3; 2.
Pfam; PF00208; Sorb; 1.
PFAMTS; PR00499; P67PHOX.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS50002; SH3; 2.
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060593;
01-AUG-1998
01-AUG-1998
01-MAR-2001
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Homo sapiens (Human).
Homo sapiens (Human).
'arvota; Metazoa; Chordata; (
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MEDLINE=97362243; PubMed=9211900;
Wang B., Golemis E.A., Kruh G.D.;
Wang B., a multiple Src homology 3
"ArgBP2, a multiple Src homology 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang B., Golemis E.A., Kruh Submitted (FEB-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ArgBP2, a multiple Src homology 3 domain-containing, Arg/Abl-interacting protein, is phosphorylated in v-Abl-transformed celocalized in stress fibers and cardiocyte 2-disks."; D. Biol. Chem. 272:17542-17550(1997).
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QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN
                                                                                                                                                                                                                                                                                          SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP---
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                                                                                          LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP
                                                                                                                                                         TPEKEKLPA---
                                                                                                                                                                                                DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
                                                                                                                                                                                                                                               SRTSPGRVDLPGSSTTLTKSF--TSSSPSSPSRAKDRESPRSYSSTLTDMGRSAPRERRG
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72; Conserv
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                                                                                                                                                                                                                                                                                                                                         29;
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EMBL/GenBank/DDBJ
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ARGBP2B (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                            Score 173;
Pred. No. 3
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3.7e-06;
~ 92;
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01-AUG-1998 (TrEMBLrel. 07, !
01-MAR-2001 (TrEMBLrel. 16, .
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Mammalia; Eutheria;
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PRODOM; PD016158; -; 1.
PROSITE; PS50002; SH3; 3.
SMART; SM00326; SH3; 1.
SEQUENCE 666 AA; 74803 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang B., Golemis E.A., Kruh G.D.; submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF049884; ARC05508.1; ... HSSP; P29354; IGRI.
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                                                                                                                                        VSGQW-EGECNG--KRGHFPFTHVRLLDQQNPD-EDF 306
                                                                                                                                                                                                                                              QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN 273
                                                                                                                                                                                                                                                                                                                                                     LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                 TPEKEKLPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP-----PGVSPSRLRIG
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                                                                                    VDQNWYEGKIPGTNRQGIFPVSYVEVVKKNTKGAEDY
                                                                                                                                                                                                                                                                                                              LSFKKGDTVYILRKIDQNWYEGE-HHGRVGIFPISYVEKLTP
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72; Conserv
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                                                                                                                                                                                                    AQPA--RPPPPAQPGEI-GEAIAKYNFNADTNVELSLRKGDRVILLK-R 536
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نم. ع.ز
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AC Q90
AC
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042287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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RAR PACE
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Best Local S
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InterPro: IPRO0145; ...
InterPro: IPRO0145; ...
InterPro: IPRO03127; ...
Pfam: PF00018; SH3; 3.
Pfam: PF00208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PR50002; SH3; 3.
SMART; SM00459; Sorb; 1.
Hypothetical protein.
SEQUENCE 816 AA; 90201 MW;
                                                                                                                         042287;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAR-2001 (TrEMBLrel. 1
INTERSECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UFT2;
Q9UFT2;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYPOL...
DKFZP586P1422.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 90.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koehrer K., Beyer A., Mewes
Submitted (SEP-1999) to the
EMBL; AL117472; CAB55947.1;
HSSP; Q60631; IGBQ.
                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
SEQUENCE FROM Hoffman N.G.,
                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 RDSSTSPGDYVLSVSENSRVSHYIINSSGPRP-----PVPPSPAQPPPGVSPSRLRIG
                                                                                                                                                                                                                                                                                                                                                                                                                                  LPFKKGDILRIRDKPEBQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP 213
                                                                                                                                                                                                                                                                                                        DQEFDSLPALLEFYKIHYLDTTTLIEFVARSRQGSGVILRQEEAEYVRALFDFNGNDEED 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESDGAPGD--LTSLENERQIYKSVLEGGDIPLQGLSGLKRPSSSASTKDSESPR-----
                                                                                                                                                                                                                                                                                      VDENWYEGRIPGTSRQGIFPITYVDVIKRPLVKNP
                                                                                                                                                                                                                                                                                                                                                                                   QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN
                                                                                                                                                                                                                                                                                                                                                                                                                 LPLQKGDIVYIYKQIDQNWYEGE-HHGRVGIFPRTYIELLPPAEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein.
816 AA; 90201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                            PRELIMINARY;
N.A.
Hardison
                                                                                                                                                                                                                                                                                                                                                    AQPKKLTPVQVLE----YGEAIAKFNFNGDTQVEMSFRKGERITLLR-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.0%;
 N.L.,
                                                                                                                                           05,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.W., Gassenhuber
EMBL/GenBank/DDBJ
                                                                                                                                           Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 170; DB 4;
Pred. No. 9.1e-06;
4; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
   Yamabhai M.,
                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFFE6647DC7730D4 CRC64;
                                                                                                                                                            sequence update)
                                                                                                                                                                                                             1270
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                                                                                                                                                                                                                                                                                           716
                                                                                                                                                                                                                                                                                                                        302
     Kay
                                                                               Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100;
                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J., Wiemann
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                  Pipidae;
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035413
                                                                                                                                                                                                                                                                                                                                                               В
  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                       InterPro; IPR000822; -.
InterPro; IPR001452; -.
InterPro; IPR00117; -.
InterPro; IPR00117; -.
Pfam; PF00018; SH3; 3.
Pfam; PF02018; SGTb; 1.
PRINTS; PR00452; SH3DOMAIN.
PRODOM; PD016158; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SMUUU,,
SMART; SMUUU,,
Calcium-binding.
Calcium-binding.
1270 AA; 143670 MW;
                                                                                                                                                                                                                                                                                      035413;
035413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002048; -.
Pfam; PF00018; SH3; 5.
Pfam; PF00036; efhand; 2.
 PROSITE;
                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAR-2001 (TrEMBLrel. 16, Last annotation updat
SH3-CONTAINING PROTEIN P4015.
                                                                                                                                                                                                                                                                                                                                                                1126
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                                                                                                            Ide N., Takeuchi M., Hata Y
Submitted (SEP-1997) to the
EMBL; AF026505; AAB81527.1;
HSSP; P29354; IGRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000261; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF032118;
HSSP; P29355; 1
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001452; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                        QQNPDE 304
                                                                                                                                                                                                                                                                                                                                                                                                               --SYAATAPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTN 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYIINSSGP
                                                                                                                                                                                                                                                                                                                                                                KSTPTE 1131
                                                                                                                                                                                                                                                                                                                                                                                                                             PNAYDKTA---LALEVGELVKVTKINVSGQWEGE--CNGKR---GHFPFTHVRLL----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -qs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQQDMWWFGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPKDSEAAG - - SGGKTGS
 PS50002;
PS00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OCT-1997) to the EMBL/GenBank/DDBJ databases. ARITY: TO EF-HAND FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYI-SMYTYESNEQGDLTFQQGDLI-VVIKKDGDMWTGTVGE-KTGVFPSNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ASLKRVSSPAFK--PAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1SEM
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-; 1,
SH3; 3.
ZINC_FINGER_C2H2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.7%;
                                                                                                                                    Hata Y.,
to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VQGQK-GWF-----PKSYVKLISGPLRKSTSIDSTSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_2
                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 165; DB 13;
Pred. No. 4.3e-05;
Pred. No. 4.3e-05;
                                                                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                 Takai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EA940C1F6B6A6858 CRC64;
                                                                                                                                                                                                                                                                                                   1196
                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                  Muridae; Murinae;
                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LGKKPEIAQVIA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 114;
                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----QGE--
                                                                                                                                                                                                  Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT
Q9P7E8
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SQ
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                    Ω
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                                                                                                                  Ωy
                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                    SQUE DE RECEPTION 
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Best Local S
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                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00018; SH3; 2.
Pfam; PF00018; SH3; 2.
Pfam; PF00241; cofilin_ADF; 1.
PRINTS; PR00499; P67PHOX.
PRINTS; PR01217; PRTCHEXTENSN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR00108; -.
InterPro; IPR001452; -.
InterPro; IPR002108; -.
InterPro; IPR002955; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9P7E8 PRELIMINARY; PRT; 857 AA.
G9P7EB;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updatace)
ACTIN BIOLING PROTEIN WITH SH3 DOMAINS.
SPAPJ760.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00326; SH3; SEQUENCE 1196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-972H-;
Harris D., Wood V., Rajandre
Submitted (MAR-2000) to the
EMBL; AL162631; CAB83085.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088 SYVEVVKRNTKGSEDY 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQW-EGECNG--KRGHFPF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GE-HHGRVGIFPISYVEKLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDLGRSVSRERRGTP----EKEVKLPAKAVYDFKAQTSKELSFKKGDTVYILRKIDQNWYE 998
GKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVQPGEI-GEAIAKYNFNADTNVELSLRKGDRIILLK-RVDQNWYEGKIPGTNRQGIFPV 108
                                                                        --QVGGDVKATEHTQPTKTPAIVIYDYSPEEENEIELVENEQIQILEFVDDGWWLGENSK
                                                                                                                  SRQGSGVILRQEEAEYVR----ALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSE 179
                                                                                                                                                                         SVPQPPAAPVVPEVPSVPQPPAVPVVPEAGQLNEPVVPPLPPH------DETQ--EP---
                                                                                                                                                                                                                     SGPRPP----VPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR
                                                                                                                                                                                                                                                                                                                                                                                                 SM00102;
NCE 857 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 29.1 57; Conservative
                                                                                                                                                                                                                                                                         l Similarity
57; Conserv
                                                                                                                                                                                                                                                                       9.7%;
ilarity 23.8%;
Conservative 3
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134052 MW;
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                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                    Score 163.5;
Pred. No. 3.4e
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    М.А.,
                                                                                                                                                                                                                                                                                                                                                                                                    247EFA78BAFE7097 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell B.G
                                                                                                                                                                                                                                                                         3.4e-05;
nes 87;
                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                             857;
                                                                                                                                                                                                                                                                            61;
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RESULT
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AC Q9
DT Q1
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Search completed:
Job time: 177 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Lin W.S., Chuang L.M.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF136380; AAD27647.1; -.

R HSSP; Q60631; 1GBQ.

R InterPro; IPR00108; -.

R InterPro; IPR001452; -.

R Pfam; pf00018; SH3; 3.

R Pfam; pf00208; Sorb; 1.

R Pfam; PF02208; Sorb; 1.

R PFANYTS; PR00499; P67PHOX.

R PRINTS; PR00499; P67PHOX.

R PRINTS; PR00492; SH3DOWAIN.

R PROSITE; PS50002; SH3; 1.

R SMART; SM00326; SH3; 1.

Q SEQUENCE 684 AA; 76341 NM; 2274E632BB07329C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%;
Best Local Similarity 25.0%;
Matches 67; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Y338 PRELIMINARY; PRT; 684 AA.
Q9Y338;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SH3P12 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                802
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                                                                                                                                                 770 GQQGLFPSNYVE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 PALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEEDLFFKKGD 160
                                                                                                                                                                                                                                                                                   506
                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 RESDGAPGD--LTSLENESQIYKSVLEGGVIPLQDLSGLKRPSSSASTKNSESPRHF--I 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 RDSSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSL 100
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                                                                                                                                                                                                                                                                               ----AQPKKLTPVQVLE----YGEAIAKFNFNGDTQVEMSFRKGERITLLR-QVDENWYE 556
                                                                                                                                                                                                                                                                                                                                    PGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQW-E 279
                                                                                                                                                                                                                                                                                                                                                                                                   ILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA------DYLEST---EEFIRRRHD------DKEMRPARAKEDFKAQTLKELPLQKGD 468
                             September 27, 2001, 16:43:09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %; Score 163; DB 4; Length 684
%; Pred. No. 2.8e-05;
40; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AEPQAGGP---
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